Figure 1:

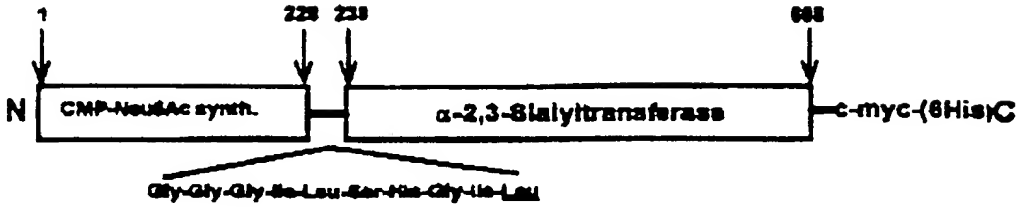
1
228
239
668
N
CMP-NeuSAc synth.
α-2,3-Sialyltransferase
c-myc-(6His)C
Gly-Gly-Gly-Ile-Leu-Ser-His-Gly-Ile-Leu

Figure 2

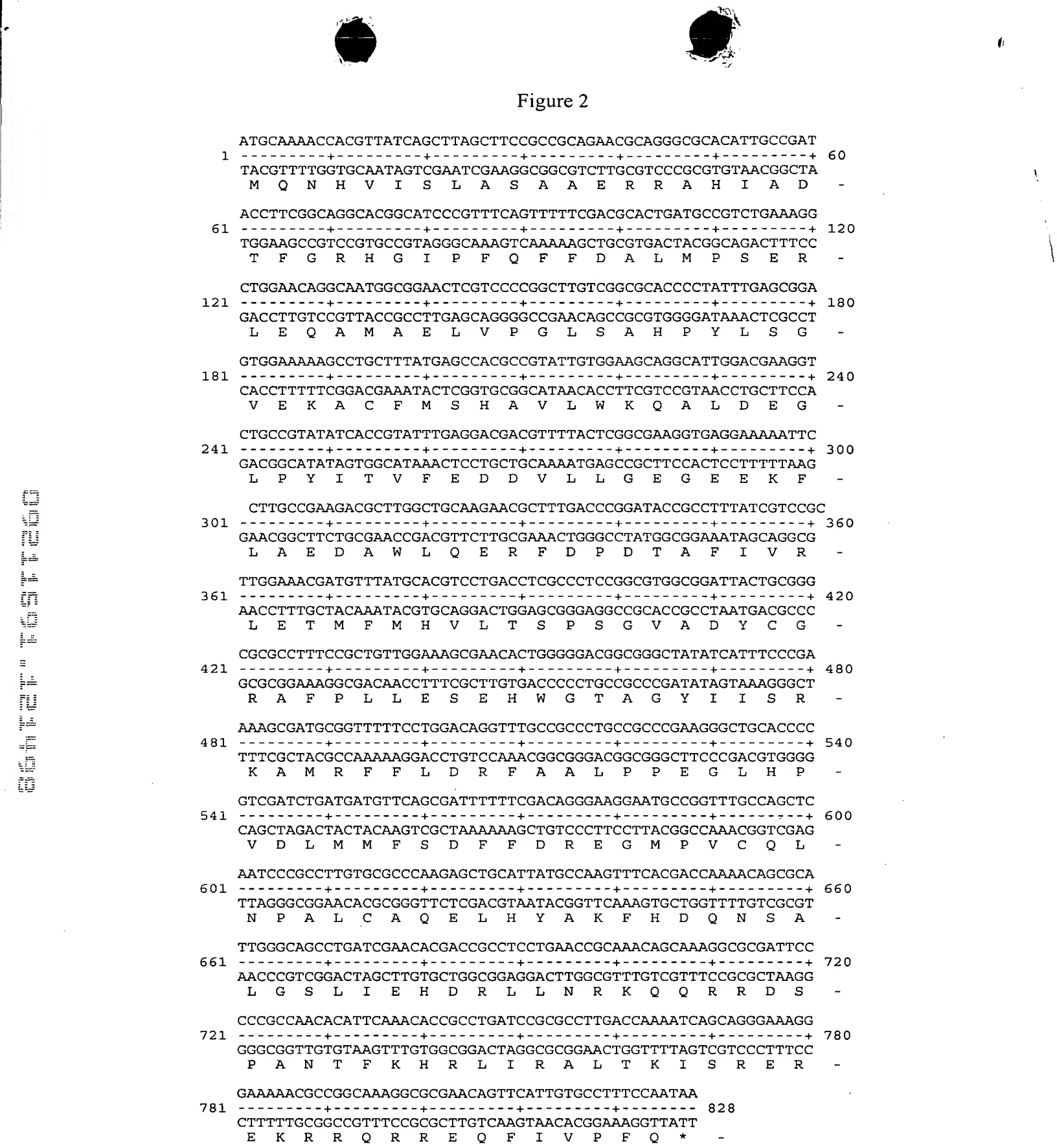
ATGCAAAACCACGTTATCAGCTTAGCTTCCGCCGCAGAACGCAGGGCGCACATTGCCGAT
1 60
TACGTTTTGGTGCAATAGTCGAATCGAAGGCGGCGTCTTGCGTCCCGCGTGTAACGGCTA
M Q N H V I S L A S A A E R R A H I A D -
ACCTTCGGCAGGCACGGCATCCCGTTTCAGTTTTTCGACGCACTGATGCCGTCTGAAAGG
61 120
TGGAAGCCGTCCGTGCCGTAGGGCAAAGTCAAAAAGCTGCGTGACTACGGCAGACTTTCC
T F G R H G I P F Q F F D A L M P S E R -
CTGGAACAGGCAATGGCGGAACTCGTCCCCGGCTTGTCGGCGCACCCCTATTTGAGCGGA
121 180
GACCTTGTCCGTTACCGCCTTGAGCAGGGGCCGAACAGCCGCGTGGGGATAAACTCGCCT
L E Q A M A E L V P G L S A H P Y L S G -
GTGGAAAAAGCCTGCTTTATGAGCCACGCCGTATTGTGGAAGCAGGCATTGGACGAAGGT
181 240
CACCTTTTTCGGACGAAATACTCGGTGCGGCATAACACCTTCGTCCGTAACCTGCTTCCA
V E K A C F M S H A V L W K Q A L D E G -
CTGCCGTATATCACCGTATTTGAGGACGACGTTTTACTCGGCGAAGGTGAGGAAAAATTC
241 300
GACGGCATATAGTGGCATAAACTCCTGCTGCAAAATGAGCCGCTTCCACTCCTTTTTAAG
L P Y I T V F E D D V L L G E G E E K F -
CTTGCCGAAGACGCTTGGCTGCAAGAACGCTTTGACCCGGATACCGCCTTTATCGTCCGC
301 360
GAACGGCTTCTGCGAACCGACGTTCTTGCGAAACTGGGCCTATGGCGGAAATAGCAGGCG
L A E D A W L Q E R F D P D T A F I V R -
TTGGAAACGATGTTTATGCACGTCCTGACCTCGCCCTCCGGCGTGGCGGATTACTGCGGG
361 420
AACCTTTGCTACAAATACGTGCAGGACTGGAGCGGGAGGCCGCACCGCCTAATGACGCCC
L E T M F M H V L T S P S G V A D Y C G -
CGCGCCTTTCCGCTGTTGGAAAGCGAACACTGGGGGACGGCGGGCTATATCATTTCCCGA
421 480
GCGCGGAAAGGCGACAACCTTTCGCTTGTGACCCCCTGCCGCCCGATATAGTAAAGGGCT
R A F P L L E S E H W G T A G Y I I S R -
AAAGCGATGCGGTTTTTCCTGGACAGGTTTGCCGCCCTGCCGCCCGAAGGGCTGCACCCC
481 540
TTTCGCTACGCCAAAAAGGACCTGTCCAAACGGCGGGACGGCGGGCTTCCCGACGTGGGG
K A M R F F L D R F A A L P P E G L H P -
GTCGATCTGATGATGTTCAGCGATTTTTTCGACAGGGAAGGAATGCCGGTTTGCCAGCTC
541 600
CAGCTAGACTACTACAAGTCGCTAAAAAAGCTGTCCCTTCCTTACGGCCAAACGGTCGAG
V D L M M F S D F F D R E G M P V C Q L -
AATCCCGCCTTGTGCGCCCAAGAGCTGCATTATGCCAAGTTTCACGACCAAAACAGCGCA
601 660
TTAGGGCGGAACACGCGGGTTCTCGACGTAATACGGTTCAAAGTGCTGGTTTTGTCGCGT
N P A L C A Q E L H Y A K F H D Q N S A -
TTGGGCAGCCTGATCGAACACGACCGCCTCCTGAACCGCAAACAGCAAAGGCGCGATTCC
661 720
AACCCGTCGGACTAGCTTGTGCTGGCGGAGGACTTGGCGTTTGTCGTTTCCGCGCTAAGG
L G S L I E H D R L L N R K Q Q R R D S -
CCCGCCAACACATTCAAACACCGCCTGATCCGCGCCTTGACCAAAATCAGCAGGGAAAGG
721 780
GGGCGGTTGTGTAAGTTTGTGGCGGACTAGGCGCGGAACTGGTTTTAGTCGTCCCTTTCC
P A N T F K H R L I R A L T K I S R E R -
GAAAAACGCCGGCAAAGGCGCGAACAGTTCATTGTGCCTTTCCAATAA
781 828
CTTTTTGCGGCCGTTTCCGCGCTTGTCAAGTAACACGGAAAGGTTATT
E K R R Q R R E Q F I V P F Q * -

Figure 3

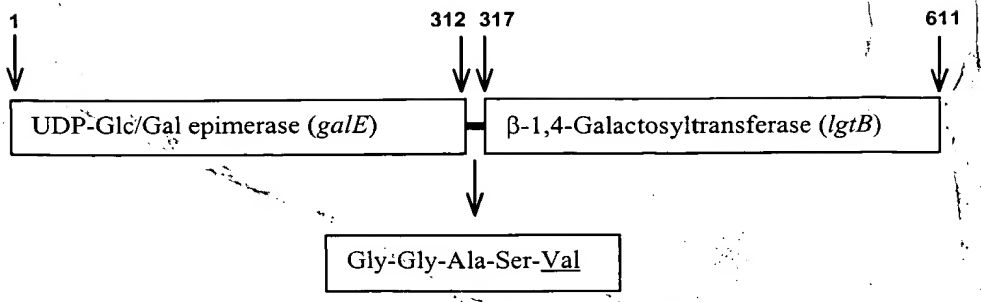
1
312
317
611
UDP-Glc/Gal epimerase (galE)
β-1,4-Galactosyltransferase (lgtB)
Gly-Gly-Ala-Ser-Val

Figure 4

A. 5' primer for amplification of *galE* for insertion into pCW at the BamHI site

5' GGGACA***GGATCC***ATCGATGCTTAGGAGGTCAT**ATG**GCAATTTTAGTATTAGGTGGAGC 3'
BamHI Met

B. 3' primer for amplification of *galE* for fusion with *lgtB* insertion into pCW

5' GGGGGG***GCTAGCGCCGCC***TCCTCGATCATCGTACCCTTTTGG 3'
NheI Gly Gly

C. 5' primer for amplification of *lgtB* for fusion with the 3' end of *galE*.

5' GGGGGG***GCTAGCGTG***CAAAACCACGTTATCAGCTTAGC
NheI Val

D. 3' primer for amplification of *lgtB* for fusion with *galE* and insertion into pCW

5' GGGGGG***GTCGAC***CTATTATTGGAAAGGCACAATGAACTGTTCGCG
SalI

E. Junction region of the *galE-lgtB* fusion

galE NheI *lgtB*

5'CCA AAA GGG TAC GAT GAT CGA GGA GGC GGA *GCT AGC* GTG CAA AAC CAC GTT ATC AGC TTA GCT 3'
3'GGT TTT CCC ATG CTA CTA GCT CCT CCG CCT *CGA TCG* CAC GTT TTG GTG CAA TAG TCG AAT CGA 5'
P K G Y D D R G G G A S V Q N H V I S L A